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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jiang, Min
Potter, Andrew A.
MacLachlan, Philip R.
- (ii) TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Reed & Robins LLP
 - (B) STREET: 285 Hamilton Avenue, Suite 200
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94301
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/658,277
 - (B) FILING DATE: 05-JUN-1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Robins, Roberta L.
 - (B) REGISTRATION NUMBER: 33,208
 - (C) REFERENCE/DOCKET NUMBER: 9000-0030
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 327-3400
 - (B) TELEFAX: (415) 327-3231

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1191 base pairs
- (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 157..924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATGAACATA AAATAAAAAT TAATAATTAT ATATTTTTTAT GATAATCACA TATATTTGAC	60
TTAAAAAAT TGTTACTGTA TGATACAGGC ATAAGTACTT ATTTATTTTA TAGATTGCAA	120
TTTATAAACA ATTATATTTT TCAAAGAGGA ATGCTT ATG GAA TTC AAA AAG TTA	174
Met Glu Phe Lys Lys Leu	
1 5	
CTT TAT TTA ACT GGT TCA ATC GCA GGA ATT ACT TTA TTT TCC CCA ATT	222
Leu Tyr Leu Thr Gly Ser Ile Ala Gly Ile Thr Leu Phe Ser Pro Ile	
10 15 20	
TTA ACA AGT GTC CAA GCA AAT CAA ATA AAT GTT AGT CAA CCA TCT AAT	270
Leu Thr Ser Val Gln Ala Asn Gln Ile Asn Val Ser Gln Pro Ser Asn	
25 30 35	
AAT GAA AGT AAT GTT ATT TCA CAG AAA AAA GAA GAA ATT GAT AAT AGT	318
Asn Glu Ser Asn Val Ile Ser Gln Lys Lys Glu Glu Ile Asp Asn Ser	
40 45 50	
CTA AAT CAG GAA AGT GCT CAA CTA TAT GCC TTG AAA GAA GAT GTT AAA	366
Leu Asn Gln Glu Ser Ala Gln Leu Tyr Ala Leu Lys Glu Asp Val Lys	
55 60 65 70	
GGA ACT GAG AAA GAA CAA TCA GTT AAT TCA GCA ATT TCA GCT GTT GAA	414
Gly Thr Glu Lys Glu Gln Ser Val Asn Ser Ala Ile Ser Ala Val Glu	
75 80 85	
AAT TTA AAA ACT TCA CTT AGA GCT AAT CCT GAA ACA ATT TAT GAT TTA	462
Asn Leu Lys Thr Ser Leu Arg Ala Asn Pro Glu Thr Ile Tyr Asp Leu	
90 95 100	
AAT TCG ATT GGA ACA AGA GTA GAA GCA ATC TCT GAC GTG ATT CAA GCA	510
Asn Ser Ile Gly Thr Arg Val Glu Ala Ile Ser Asp Val Ile Gln Ala	
105 110 115	
ATT GTT TTT TCA ACG CAA CAG TTA ACA AAT AAA GTT GAT CAA GCT CAC	558
Ile Val Phe Ser Thr Gln Gln Leu Thr Asn Lys Val Asp Gln Ala His	
135 140 145 150	

CCA	TTT	GCT	TCA	AAT	GAA	TCC	ATT	AAA	GGG	CAA	GTC	GAA	GCT	GTT	AAA	654
Pro	Phe	Ala	Ser	Asn	Glu	Ser	Ile	Lys	Gly	Gln	Val	Glu	Ala	Val	Lys	
				155					160					165		
CAA	GTG	CAA	GCG	ACT	GTG	CTT	ACC	TAT	CCC	GAT	TTG	CAG	CCT	ACG	GAT	702
Gln	Val	Gln	Ala	Thr	Val	Leu	Thr	Tyr	Pro	Asp	Leu	Gln	Pro	Thr	Asp	
			170					175					180			
AGA	GCA	ACT	ATT	TAC	GTT	AAA	TCA	AAA	TTA	GAC	AAG	CTT	ATT	TGG	CAA	750
Arg	Ala	Thr	Ile	Tyr	Val	Lys	Ser	Lys	Leu	Asp	Lys	Leu	Ile	Trp	Gln	
		185					190					195				
ACA	AGA	ATT	ACC	AGA	GAT	CAA	AAA	GTT	CTT	AAT	GTA	AAG	AGT	TTT	GAA	798
Thr	Arg	Ile	Thr	Arg	Asp	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Phe	Glu	
	200					205					210					
GTT	TAT	CAT	CAA	TTA	AAT	AAA	GCT	ATC	ACA	CAT	GCA	GTA	GGT	GTA	CAA	846
Val	Tyr	His	Gln	Leu	Asn	Lys	Ala	Ile	Thr	His	Ala	Val	Gly	Val	Gln	
215				220					225					230		
TTA	AAT	CCA	ACT	GTA	ACA	GTT	GCA	CAA	GTT	GAC	CAA	GAA	ATC	AAA	GTG	894
Leu	Asn	Pro	Thr	Val	Thr	Val	Ala	Gln	Val	Asp	Gln	Glu	Ile	Lys	Val	
			235					240					245			
CTA	CAA	GAA	GCA	TTA	AAT	ACT	GCT	CTA	CAG	TAAGGTAGAG	ATTGAATTGA					944
Leu	Gln	Glu	Ala	Leu	Asn	Thr	Ala	Leu	Gln							
		250					255									
CGTATTAAAA	AGGACTGGAA	TTTATTAATT	TCAGTCCTTT	AGAATTTT	TTTAGCTGAT											1004
TTACTTGTTG	AAGAGATTG	GTGGAAAATC	AAGTACCATA	CTTCATTTCT	CCTCCAAATA											1064
CTTGATGTC	GATTCCCTTC	TAAACATAG	CTAATTAGTT	TAGTTTTCTG	GCTAATAGAT											1124
TGTACATGAA	ATTGTTCAAA	ATTACTAGGG	TAAAAGGTTT	TTCTTTTAT	AAATTCATCA											1184
TGACTAT																1191

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Phe	Lys	Lys	Leu	Leu	Tyr	Leu	Thr	Gly	Ser	Ile	Ala	Gly	Ile	1	5	10	15
Thr	Leu	Phe	Ser	Pro	Ile	Leu	Thr	Ser	Val	Gln	Ala	Asn	Gln	Ile	Asn	20	25	30	
Val	Ser	Gln	Pro	Ser	Asn	Asn	Glu	Ser	Asn	Val	Ile	Ser	Gln	Lys	Lys	35	40	45	
Glu	Glu	Ile	Asp	Asn	Ser	Leu	Asn	Gln	Glu	Ser	Ala	Gln	Leu	Tyr	Ala	50	55	60	
Leu	Lys	Glu	Asp	Val	Lys	Gly	Thr	Glu	Lys	Glu	Gln	Ser	Val	Asn	Ser	65	70	75	80
Ala	Ile	Ser	Ala	Val	Glu	Asn	Leu	Lys	Thr	Ser	Leu	Arg	Ala	Asn	Pro	85	90	95	
Glu	Thr	Ile	Tyr	Asp	Leu	Asn	Ser	Ile	Gly	Thr	Arg	Val	Glu	Ala	Ile	100	105	110	
Ser	Asp	Val	Ile	Gln	Ala	Ile	Val	Phe	Ser	Thr	Gln	Gln	Leu	Thr	Asn	115	120	125	
Lys	Val	Asp	Gln	Ala	His	Ile	Asp	Met	Gly	Phe	Ala	Ile	Thr	Lys	Leu	130	135	140	
Leu	Ile	Arg	Ile	Ala	Asp	Pro	Phe	Ala	Ser	Asn	Glu	Ser	Ile	Lys	Gly	145	150	155	160
Gln	Val	Glu	Ala	Val	Lys	Gln	Val	Gln	Ala	Thr	Val	Leu	Thr	Tyr	Pro	165	170	175	
Asp	Leu	Gln	Pro	Thr	Asp	Arg	Ala	Thr	Ile	Tyr	Val	Lys	Ser	Lys	Leu	180	185	190	
Asp	Lys	Leu	Ile	Trp	Gln	Thr	Arg	Ile	Thr	Arg	Asp	Gln	Lys	Val	Leu	195	200	205	
Asn	Val	Lys	Ser	Phe	Glu	Val	Tyr	His	Gln	Leu	Asn	Lys	Ala	Ile	Thr	210	215	220	
His	Ala	Val	Gly	Val	Gln	Leu	Asn	Pro	Thr	Val	Thr	Val	Ala	Gln	Val	225	230	235	240

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met 1	Glu	Phe	Lys	Lys 5	Leu	Leu	Tyr	Leu	Thr 10	Gly	Ser	Ile	Ala	Gly 15	Ile
Thr	Leu	Phe	Ser 20	Pro	Ile	Leu	Thr	Ser 25	Val	Gln	Ala	Asn	Gln 30	Ile	Asn
Val	Ser	Gln 35	Pro	Ser	Asn	Asn	Glu 40	Ser	Asn	Val	Ile	Ser 45	Gln	Lys	Lys
Glu	Glu 50	Ile	Asp	Asn	Ser	Leu 55	Asn	Gln	Glu	Ser	Ala 60	Gln	Leu	Tyr	Ala
Leu 65	Lys	Glu	Asp	Val	Lys 70	Gly	Thr	Glu	Lys	Glu 75	Gln	Ser	Val	Asn	Ser 80
Ala	Ile	Ser	Ala	Val 85	Glu	Asn	Leu	Lys	Thr 90	Ser	Leu	Arg	Ala	Asn 95	Pro
Glu	Thr	Ile	Tyr 100	Asp	Leu	Asn	Ser	Ile 105	Gly	Thr	Arg	Val	Glu 110	Ala	Ile
Ser	Asp	Val 115	Ile	Gln	Ala	Ile	Val 120	Phe	Ser	Thr	Gln	Gln 125	Leu	Thr	Asn
Lys	Val 130	Asp	Gln	Ala	His	Ile 135	Asp	Met	Gly	Phe	Ala 140	Ile	Thr	Lys	Leu
Leu 145	Ile	Arg	Ile	Ala	Asp 150	Pro	Phe	Ala	Ser	Asn 155	Glu	Ser	Ile	Lys	Gly 160
Gln	Val	Glu	Ala	Val	Lys	Gln	Val	Gln	Ala 165	Thr	Val	Leu	Thr 175	Tyr	Pro

Asp	Lys	Leu	Ile	Trp	Gln	Thr	Arg	Ile	Thr	Arg	Asp	Gln	Lys	Val	Leu
		195					200					205			
Asn	Val	Lys	Ser	Phe	Glu	Val	Tyr	His	Gln	Leu	Asn	Lys	Ala	Ile	Thr
		210				215					220				
His	Ala	Val	Gly	Val	Gln	Leu	Asn	Pro	Thr	Val	Thr	Val	Ala	Gln	Val
225					230					235					240
Asp	Gln	Glu	Ile	Lys	Val	Leu	Gln	Glu	Ala	Leu	Asn	Thr	Ala	Leu	Gln
				245					250						255

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp	Gln	Val	Thr	Thr	Pro	Gln	Val	Val	Asn	His	Val	Asn	Ser	Asn	Asn
1				5					10					15	
Gln	Ala	Gln	Gln	Met	Ala	Gln	Lys	Leu	Asp	Gln	Asp	Ser	Ile	Gln	Leu
		20					25						30		
Arg	Asn	Ile	Lys	Asp	Asn	Val	Gln	Gly	Thr	Asp	Tyr	Glu	Lys	Pro	Val
	35					40						45			
Asn	Glu	Ala	Ile	Thr	Ser	Val	Glu	Lys	Leu	Lys	Thr	Ser	Leu	Arg	Ala
	50					55					60				
Asn	Ser	Glu	Thr	Val	Tyr	Asp	Leu	Asn	Ser	Ile	Gly	Ser	Arg	Val	Glu
65				70						75					80
Ala	Leu	Thr	Asp	Val	Ile	Glu	Ala	Ile	Thr	Phe	Ser	Thr	Gln	His	Leu
				85					90					95	
Lys	Leu	Val	Thr	Arg	Leu	Leu	Asp	Leu	Val	Thr	Val	Thr	Val	Thr	Val
		115					120						125		

[illegible]